AMENDMENTS TO THE SPECIFICATION

Page 20

Line 1, please replace page 20 with the following new amended page 20:

-- **Example 2: GENERATING PRIMER SEQUENCES using method as DESCRIBED -- COMPUTER SIMULATION**

(A)

GENE:	AGAMOUS
FUNCTION:	TRANSCRIPTION FACTOR
DOMAIN:	MADS BOX

SEQ ID NO: 1	AA SEQUENCE:	G	R	G	K	I	E	I	K	R	I	E		
SEQ ID NO: 2	Predicted NT:	GGG	AGG	GGC	AAG	AUC	GAG	AUC	AAG	CGC	AUC	GAG		
SEQ ID NO: 3	Maize	GGG	AGa	GGC	AAG	AUC	GAG	AUC	AAG	CGC	AUC	GAG		32/33
SEQ ID NO: 4	Rice	GGG	AGG	GGg	AAG	AUC	GAG	AUC	AAG	CGg	AUC	GAG		31/33
SEQ ID NO: 5	Arabidopsis	GGG	AGA	GGA	AAG	AUC	GAA	AUC	AAA	CGG	AUC	GAG	(M)	28/33
													(R)	29/33

(B)

GENE:	APETALA1
FUNCTION:	TRANSCRIPTION FACTOR
DOMAIN:	MADS BOX

SEQ ID NO: 6	AA SEQUENCE:	R	I	E	N	K	I	N	R	Q	V	T	F		
SEQ ID NO: 7	Predicted NT:	AGG	AUC	GAG	AAC	AAG	AUC	AAC	AAG	CAG	GUG	ACC	UUC		
SEQ ID NO: 8	Maize	cGG	AUC	GAG	AAC	AAG	AUC	AAC	cGG	CAG	GUg	ACC	UUC		33/36
SEQ ID NO: 9	Rice	AGG	AUC	GAG	AAC	AAG	AUC	AAC	cGG	CAG	GUG	ACg	UUC		34/36
SEQ ID NO: 10	Arabidopsis	AGG	AUA	GAG	AAC	AAG	AUC	AAA	AGA	CAA	GUG	ACA	UUC	(M)	29/36
													(R)	30/36

(C)

GENE:	APETALA2
FUNCTION:	TRANSCRIPTION FACTOR
DOMAIN:	AP2 DOMAIN

SEQ ID NO: 11	AA SEQUENCE:	G	R	W	E	S	H	I	W	D	C		
SEQ ID NO: 12	Predicted NT:	GGC	AGG	UGG	GAG	UCC	CAC	AUC	UGG	GAC	UGC		
SEQ ID NO: 13	Maize	GGC	cGc	UGG	GAa	UCC	CAC	AUC	UGG	GAC	UGC		27/30
SEQ ID NO: 14	Arabidopsis	GGA	AGA	UGG	GAA	UCU	CAU	AUU	UGG	GAC	UGU	(M)	23/30 --

Page 21

Please replace page 21 with the following new amended page 21:

-- **Example 3: SPECIFICITY OF CODON ADJUSTED PRIMERS**
The following example illustrates the specificity of codon adjusted primer pairs. Primers 1 and 2 represent primers taken directly from the sequence of the template polynucleotide. Primers 1' and 2' are primers wherein the sequence has been codon adjusted for monocots according to the invention. These primers were used to identify target polynucleotides from corn and rice.

Primer 1

SEQ ID NO: 15	AA SEQUENCE	D C G L Q V	
SEQ ID NO: 16	Coding Sequence:	5' G GAC TGT GGG AAA CAA GTT TA 3'	
SEQ ID NO: 17	Primer 1 Sequence:	5' G GAC TGT GGG AAA CAA GTT TA 3'	
SEQ ID NO: 18	Primer 1' (Codon Adjusted Sequence):	5' G GAC TGC GGG AAG CAG GTG TA 3'	17/21
	%Sequence Identity to Primer 1:	81%	

Primer 2

SEQ ID NO: 19	AA SEQUENCE	K Y R G V T L	
SEQ ID NO: 20	Coding Sequence:	5' AAG TAT AGA GGT GTC ACT TTG CA 3'	
SEQ ID NO: 21	Complement	3' TTC ATA TCT CCA CAG TGA AAC GT 5'	
SEQ ID NO: 22	Primer 2 Sequence:	5' TG CAA AGT GAC ACC TCT ATA CTT 3'	
SEQ ID NO: 23	Codon Adjusted Sequence:	5' AAG TAC AGG GGC GTC ACC TTG CA 3'	
SEQ ID NO: 24	Complement	3' TTC ATG TCC CCG CAG TGG AAC GT 5'	
SEQ ID NO: 25	Primer 2' Sequence:	5' TG CAA GGT GAC GCC CCT GTA CTT 3'	19/23
	%Sequence Identity to Primer 2:	83% --	

Page 23

Please replace page 23 with the following new amended page 23:

-- **Example 4**

The method of the invention was used to isolate AP2-like genes from Avena sativa (oat), Oryza sativa (rice), Triticum aestivum (wheat) and Zea mays (corn). Primers 1' and 2' described in Example 3 were used in PCR using the conditions of Example 1 and genomic DNA from each plant as a source of target polynucleotides. The nucleotide and corresponding amino acid sequences of PCR-amplified products are shown below.

```
>OAT ADC GENE 489 BP  (SEQ ID NO.: 26)
TACCTAGGTGAGCTCAAATTCCCAGCTCCAGCTCCTCCTAATTAATTTCCATCTGTTCTGTGTACTGAAGTTATTTAATTTCGTCAGGTGGTTTCGACACC
GCGCACTCGGCCGCGAGGTTATAATTAATCAAGCTTCCTAGTTTGAACTTTCAACACATACTGCTCTCTCTCGATTGGATTGTACTAGCATCATGAACTGT
ACTGAAACGGGTCTTGCTCAGGGCCTACGATCGCGCGGCGATCAAGTTCCGGGGACTGGACGCCGACATCAACTTCAATCTGAGCGACTACGAGGAGGATC
TGAAGCAGGTAACTGAATAAGATCGCTTCCTCAAATGCAGCATAGATATTATCGGTGTGTGTGTGTCTGATGGGTGGTTGGTGGCCGGCCGGGCACTCTTG
TTTTTGCCAGATGAGGAACTGGACCAAGGAGGAGTTCGTGCACATCCTCCGCCGCCAGAGCACGGGGTTCGCGAGGGGGAGCTCA
```

```
>OAT ADC PROTEIN 65 aa  (SEQ ID NO: 27)
GGFDTAHSAARAYDRAAIKFRGLDADINFNLSDYEEDLKQVTNWTKEEFVHILRRQSTGFARGSS
```


```
>RICE AP2-LIKE GENE 387 BP  (SEQ ID NO: 28)
CCTAGGTAATTTCATCGAACACATCATCTTCCTCCTCTCAATCCAACGCGACATCGCCATGAACAATCTAACAAACACCTTCATCTTCTCCCAAACAATCA
CAGGTGGATTCGACACTGCTCACGCAGCTGCAAGGTAAAGAACACATCACATCATTCATCAGAACATGAGCTCTGTGTTTGTGAAGGAGATTGAGAGAATT
GAATGATGATGGATGGATGCAGGGCGTACGACAGGGCGGCGATCAAGTTCAGGGGAGTAGAGGCTGACATCAACTTCAACCTGAGCGACTACGAGGAGGAC
ATGAGGCAGATGAAGAGCTTGTCCAAGGAGGAGTTCGTGCACGTTCTCCGGCGACAGAGCACCGGCTTCTCCCGCGGCAGCTCA
```

```
>RICE ADC PROTEIN 65 aa  (SEQ ID NO: 29)
GGFDTAHAAARAYDRAAIKFRGVEADINFNLSDYEEDMRQMKSLSKEEFVHVLRRQSTGFSRGSS
```


```
>WHEAT ADC GENE 477 BP  (SEQ ID NO: 30)
CTTGGGTGGGTTTGACACTGCACATGCTGCTGCAAGGTACGTACAAATTTAATTAAGCACGTACGCAGTACATAATTGTGATGTGATCATCACCTGAACCA
CCTGTACTGCAACTCTGAAGTTATGTCTCCACTCTGTTCATTTCACCGTGCCAAATTGACCTTGGGATGTTCCGCAGGGCGTACGATCGAGCGGCGATCAA
GTTCCGCGGCGTCGACGCCGACATAAACTTCAACCTCAGCGACTACGAGGACGACATGAAGCAGGTGATCAGCAAAGCCACCAACCAGTGTTCCTCATCCA
ACCAAATTATTCAGATGCAGAGTGCATTAGTACTGTTGTTGAAACTGATGAACTGAAGAAATTCTGACTGTGTGTTGKTTGGTGGATGATCTGGATCAGAT
GAAGGGCCTGTCCAAGGAGGAGTTCGTGCACGTGCTGCGGCGGCAGAGCGCCGGCTTCTCGCGGGGCAGCTCC
```

```
>WHEAT ADC PROTEIN 65 aa  (SEQ ID NO: 31)
GGFDTAHAAARAYDRAAIKFRGVDADINFNLSDYEDDMKQVKGLSKEEFVHVLRRQSAGFSRGSS
```


```
>MAIZE ADC GENE 489 BP  (SEQ ID NO: 32)
CTTAGGTGAGCAGCAATAAGCAGATCGATCTGCAGCATAAATTTCCCGTTATTAACTAGTTCGTGATCTCGATCGAATGGCCTAATTAACCGATTCGGTGA
TCTGGCCGATGGCCAATCTACGCAGGTGGATTCGACACTGCTCATGCCGCTGCAAGGTAACGATCAATCCATCCATCCACCCTTGTCTAGCTACCCCACCG
ACCGGCCGGATTAATGGACCGCTAGTTCTCGGGACGGGCTTGCTGCAGGGCGTACGACCGAGCGGCGATCAAGTTCCGCGGCGTCGACGCCGACATAAACT
TCAACCTCAGCGACTACGACGACGATATGAAGCAGGTACATACACGAGTGTTGTTGCAGCTAGCACCGACTGAAACATCTGCTGAACGTACACTCATGGCC
TGTGCACCAGATGAAGAGCCTGTCCAAGGAGGAGTTCGTGCACGCCCTGCGGCGGCAGAGCACCGGCTTCTCCCGTGGCAGCTCC
```

```
>MAIZE ADC PROTEIN 65 aa  (SEQ ID NO: 33)
GGFDTAHAAARAYDRAAIKFRGVDADINFNLSDYDDDMKQVKSLSKEEFVHALRRQSTGFSRGSS      --
```

4

Page 24

Please replace the paragraph beginning on line 25 with the following new amended paragraph:

-- Primer 1

SEQ ID NO: 34	AA SEQUENCE					D C G L Q V
SEQ ID NO: 35	Coding Sequence:					5' G GAC TGT GGG AAA CAA GTT TA 3'
SEQ ID NO: 36	Primer Sequence:					5' G GAC TGT GGG AAA CAA GTT TA 3'

SEQ ID NO: 37   Primer 1' (Codon Adjusted Sequence): 5' G GAC TGC GGG AAG CAG GTG TA 3' --

Page 25

Please replace the paragraph beginning on page 25, line 1 and ending on line 41 with the following new amended paragraph:

-- Primer 2

SEQ ID NO: 38   AA SEQUENCE   K   Y   R   G   V   T   L

SEQ ID NO: 39   Coding Sequence: 5' AAG TAT AGA GGT GTC ACT TTG CA 3'

SEQ ID NO: 40   Complement   3' TTC ATA TCT CCA CAG TGA AAC GT 5'

SEQ ID NO: 41   Primer 2 Sequence: 5' TG CAA AGT GAC ACC TCT ATA CTT 3'

SEQ ID NO: 42   Codon Adjusted Sequence: 5' AAG TAC AGG GGC GTC ACC TTG CA 3'

SEQ ID NO: 43   Complement   3' TTC ATG TCC CCG CAG TGG AAC GT 5'

SEQ ID NO: 44   Primer 2' Sequence: 5' TG CAA GGT GAC GCC CCT GTA CTT 3'

SEQ ID NO: 45   RISZU2'-1 (5 CODONS)   5' G CAA GGT GAC GCC CCT GT   3'

SEQ ID NO: 46   RISZU2'-2 (5 CODONS)   5'   GGT GAC GCC CCT GTA CT   3'

SEQ ID NO: 47   RISZU2'-3 (4 CODONS)   5'   GT GAC GCC CCT GTA CT   3'

SEQ ID NO: 48   RISZU2'-4 (3 CODONS)   5'   GT GAC GCC CCT GT   3' --